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Fig. 9

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

Pig uricase:

Pig cDNA from 1 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003

Quality:	1493	Length:	305
Ratio:	4.895	Gaps:	0

Percent Similarity:	94.098	Percent Identity:	90.820
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Match display thresholds for the alignment(s):

	= IDENTITY
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:	= 2
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.	= 1
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Pig.pep x baboon D3H.pep

June 25, 1998 17:44 ..

Pig	1 MAHYRNDYKKNDEVEFVRTGYGKDMIKVLH1QRDGKYHSIKEVATSVQLT 50
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Bab	1 MAHYHNNYKKNDELEFVRTGYGKDMVKVLH1QRDGKYHSIKEVATSVQLT 50
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51 LSSKKDYLHGDNSDVIPTDTIKNTNVNLAKFKGIKSIEFTFAVTICEHFLS 100
--

51 LSSKKDYLHGDNSDIIPDTIKNTVHLAKFKGIKSIEAFGVNICEYFLS 100

101 SFKHVIRAQVYVEEVPWKRFEKNGVKHVHAIFIYTPGTGTHFCEVEQIRNGP 150
--

101 SFNHVIRAQVYVEEIPWKRLEKNGVKHVHAIFIYTPGTGTHFCEVEQLRSGP 150
--

151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATOVYCKWRYH 200
--

151 PVIHSGIKDLKVLKTTQSGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH 200
--

201 QGRDVDDFEATWDTVRSIVLQKFAGPYDKGEYSPSVQKTLYDIQVLTGQV 250
--

201 QC RDVDDFEATWGTIRDLVLEKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV 250
--

251 PEIEDMEISLPNIHYLNIDMSKMGLINKEEVLLPLDNPYGRITGTVKRKL 300
--

251 PEIEDMEISLPNIHYFNIDMSKMGLINKEEVLLPLDNPYGKITGTVKRKL 300
--

301 TSRL* 305

.

301 SSRL* 305

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Fig. 10

Comparison of amino acid sequence of the "original" Pig-baboon chimeric uricase ("chimera") with that of "Baboon D3H" uricase (Baboon except for His replacing Asp at amino acid 3)

"Chimera" uricase:

Pig cDNA from 1 to 674 (Apa site) and then Baboon cDNA from 675 to 915 (end)

"Baboon D3H" uricase:

"Baboon D3H" cDNA from 1 to 915 (end)

[GCG GAP program]

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1516	Length:	305
Ratio:	4.970	Gaps:	0
Percent Similarity:	95.738	Percent Identity:	92.787

Match display thresholds for the alignment(s):
 | = IDENTITY
 : = 2
 . = 1

chimera.pep x baboon D3H.pep June 25, 1998 17:18 ..

chim	1	MAHYRNDYKKNDEVEFVRTGYKGDKMKVLHIIQRDGKYHSIKEVATSVQLT	50
Bab	1	MAHYHNNYKKNDELEFVRTGYKGDKMKVLHIIQRDGKYHSIKEVATSVQLT	50
	51	LSSKKDYLHGDNSDVIPTDTIKNTVNVLAKFKGIKSIEFTFAVTICEHFLS	100
	51	LSSKKDYLHGDNSDIIPDTIKNTVHVLAKFPGIKSIEAFGVNICEYFLS	100
	101	SFKHVIRAQVYVEEPWPKRFKEKNGVKHVHAFIYTPGTGHFCEVEQIRNGP	150
	101	SFMHVIRAQVYVEEIPWKRLKEKNGVKHVHAFIYTPGTGHFCEVEQLRSGP	150
	151	PVIHSGIKDLKVLKTTQSFGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH	200
	151	PVIHSGIKDLKVLKTTQSFGFEGFIKDQFTTLPEVKDRCFATQVYCKWRYH	200
	201	QGRDVDFEATWDITVRSIVLQK FAGPYDKGEYSPSVQKTLYDIQVLSLSRV	250
	201	QCRDVDFEATWGTTIRDLVLEKFAGPYDKGEYSPSVQKTLYDIQVLSLSRV	250
	251	PEIEDMEISLPNIHYFNIDMSKMGMLINKEEVLLPLDNPYKITGTVKRKL	300
	251	PEIEDMEISLPNIHYFNIDMSKMGMLINKEEVLLPLDNPYKITGTVKRKL	300
	301	SSRL* 305	
	301	SSRL* 305	

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Fig. 11-1

Bestfit (GCG software) comparison of coding sequences of the cDNAs of Pig KS uricase ("PKS") vs. pig uricase

"Pig KS" uricase:

Pig cDNA from 1 to 864 (NdeI site) and then Baboon 865 to 915 (end)

Gap Weight: 50 Average Match: 10.000
 Length Weight: 3 Average Mismatch: -9.000

Quality: 9036 Length: 915
 Ratio: 9.875 Gaps: 0
 Percent Similarity: 99.344 Percent Identity: 99.344

Match display thresholds for the alignment(s):
 | = IDENTITY
 : = 5
 . = 1

pigKS.seq x pig.seq July 25, 1998 10:14 ..

PKS	1	ATGGCTCATTAACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTGT	50
pig	1	ATGGCTCATTAACCGTAATGACTACAAAAAGAATGATGAGGTAGAGTTGT	50
	51	CCGAACCTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAAGCGAG	100
	51	CCGAACCTGGCTATGGGAAGGATATGATAAAAGTTCTCCATATTCAAGCGAG	100
	101	ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT	150
	101	ATGGAAAATATCACAGCATTAAAGAGGTGGCAACTTCAGTGCAACTGACT	150
	151	TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAAGATGTCACTCCC	200
	151	TTGAGCTCCAAAAAGATTACCTGCATGGAGACAATTCAAGATGTCACTCCC	200
	201	TACAGACACCATCAAGAACACAGTTAACATGCTGGCGAAGTCAAAGGCA	250
	201	TACAGACACCATCAAGAACACAGTTAACATGCTGGCGAAGTCAAAGGCA	250
	251	TCAAAAGCATAGAAACTTTGCTGTGACTATCTGTGAGCATTCCCTTCT	300
	251	TCAAAAGCATAGAAACTTTGCTGTGACTATCTGTGAGCATTCCCTTCT	300
	301	TCCTTCAAGCATGTCACTCAGAGCTCAAGTCTATGTGGAAGAAGTTCTTG	350
	301	TCCTTCAAGCATGTCACTCAGAGCTCAAGTCTATGTGGAAGAAGTTCTTG	350
	351	GAAGCGTTTGAAGAATGGAGTTAACGATGTCCATGCATTATTTATA	400
	351	GAAGCGTTTGAAGAATGGAGTTAACGATGTCCATGCATTATTTATA	400